

WHAT IS CLAIMED IS:

1. A trehalose synthase protein with the following amino acid sequence:

5	Met Ser Ile Pro Asp Asn Thr Tyr Ile Glu Trp Leu Val Ser Gln	5	10	15
	Ser Met Leu His Ala Ala Arg Glu Arg Ser Arg His Tyr Ala Gly	20	25	30
	Gln Ala Arg Leu Trp Gln Arg Pro Try Ala Gln Ala Arg Pro Arg	35	40	45
10	Asp Ala Ser Ala Ile Ala Ser Val Trp Phe Thr Ala Tyr Pro Ala	50	55	60
	Ala Ile Ile Thr Pro Glu Gly Gly Thr Val Leu Glu Ala Leu Gly	65	70	75
	Asp Asp Arg Leu Trp Ser Ala Leu Ser Glu Leu Gly Val Gln Gly	80	85	90
15	Ile His Asn Gly Pro Met Lys Arg Ser Gly Gly Leu Arg Gly Arg	95	100	105
	Glu Phe Thr Pro Thr Ile Asp Gly Asn Phe Asp Arg Ile Ser Phe	110	115	120
20	Asp Ile Asp Pro Ser Leu Gly Thr Glu Glu Gln Met Leu Gln Leu	125	130	135
	Ser Arg Val Ala Ala Ala His Asn Ala Ile Val Ile Asp Asp Ile	140	145	150
	Val Pro Ala His Thr Gly Lys Gly Ala Asp Phe Arg Leu Ala Glu	155	160	165
25	Met Ala Tyr Gly Asp Tyr Pro Gly Leu Tyr His Met Val Glu Ile	170	175	180
	Arg Glu Glu Asp Trp Glu Leu Leu Pro Glu Val Pro Ala Gly Arg	185	190	195
30	Asp Ser Val Asn Leu Leu Pro Pro Val Val Asp Arg Leu Lys Glu	200	205	210
	Lys His Tyr Ile Val Gly Gln Leu Gln Arg Val Ile Phe Phe Glu	215	220	225

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	Pro Gly Ile Lys Asp Thr Asp Trp Ser Val Thr Gly Glu Val Thr	
	230	240
	Gly Val Asp Gly Lys Val Arg Arg Trp Val Tyr Leu His Tyr Phe	
	245	255
	Lys Glu Gly Gln Pro Ser Leu Asn Trp Leu Asp Pro Thr Phe Ala	
	260	270
	Ala Gln Gln Leu Ile Ile Gly Asp Ala Leu His Ala Ile Asp Val	
	275	285
10	Thr Gly Ala Arg Val Leu Arg Leu Asp Ala Asn Gly Phe Leu Gly	
	290	300
	Val Glu Arg Arg Ala Glu Gly Thr Ala Trp Ser Glu Gly His Pro	
	305	315
	Leu Ser Val Thr Gly Asn Gln Leu Leu Ala Gly Ala Ile Arg Lys	
	320	330
15	Ala Gly Gly Phe Ser Phe Gln Glu Leu Asn Leu Thr Ile Asp Asp	
	335	345
	Ile Ala Ala Met Ser His Gly Gly Ala Asp Leu Ser Tyr Asp Phe	
	350	360
20	Ile Thr Arg Pro Ala Tyr His His Ala Leu Leu Thr Gly Asp Thr	
	365	375
	Glu Phe Leu Arg Met Met Leu Arg Glu Val His Ala Phe Gly Ile	
	380	390
	Asp Pro Ala Ser Leu Ile His Ala Leu Gln Asn His Asp Glu Leu	
	395	405
25	Thr Leu Glu Leu Val His Phe Trp Thr Leu His Ala Tyr Asp His	
	410	420
	Tyr His Tyr Lys Gly Gln Thr Leu Pro Gly Gly His Leu Arg Glu	
	425	435
	His Ile Arg Glu Glu Met Tyr Glu Arg Leu Thr Gly Glu His Ala	
30	440	450
	Pro Tyr Asn Leu Lys Phe Val Thr Asn Gly Val Ser Cys Thr Thr	
	455	465

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	Ala Ser Val Ile Ala Ala Ala Leu Asn Ile Arg Asp Leu Asp Ala	
	470	475 480
	Ile Gly Pro Ala Glu Val Glu Gln Ile Gln Arg Leu His Ile Leu	
	485	490 495
	Leu Val Met Phe Asn Ala Met Gln Pro Gly Val Phe Ala Leu Ser	
	500	505 510
	Gly Trp Asp Leu Val Gly Ala Leu Pro Leu Ala Pro Glu Gln Val	
	515	520 525
10	Glu His Leu Met Gly Asp Gly Asp Thr Arg Trp Ile Asn Arg Gly	
	530	535 540
	Gly Tyr Asp Leu Ala Asp Leu Ala Pro Glu Ala Ser Val Ser Ala	
	545	550 555
	Glu Gly Leu Pro Lys Ala Arg Ser Leu Tyr Gly Ser Leu Ala Glu	
	560	565 570
15	Gln Leu Gln Arg Pro Gly Ser Phe Ala Cys Gln Leu Lys Arg Ile	
	575	580 585
	Leu Ser Val Arg Gln Ala Tyr Asp Ile Ala Ala Ser Lys Gln Ile	
	590	595 600
	Leu Ile Pro Asp Val Gln Ala Pro Gly Leu Leu Val Met Val His	
20	605	610 615
	Glu Leu Pro Ala Gly Lys Gly Val Gln Leu Thr Ala Leu Asn Phe	
	620	625 630
	Ser Ala Glu Pro Val Ser Glu Thr Ile Cys Leu Pro Gly Val Ala	
	635	640 645
25	Pro Gly Pro Val Val Asp Ile Ile His Glu Ser Val Glu Gly Asp	
	650	655 660
	Leu Thr Asp Asn Cys Glu Leu Gln Ile Asn Leu Asp Pro Tyr Glu	
	665	670 675
	Gly Leu Ala Leu Arg Val Val Ser Ala Ala Pro Pro Val Ile	
30	680	685

2. A trehalose synthase gene with the following nucleotide sequence:

GATCGCTGGC GTACTGCAGG TAGAGCAGGC GCATCGGCCC CCAGGGCGCA TCGGCCGGCT 60
 CCGCTGTGCC CTGCTGGTTC ATGAAGCGGA CGAAGCGGCC ATCGCGGAAC CGTGGACGCC 120
 ATTCGGGGCT GTCCGGGTCG CCGCTGTGCG TGAGCGTGCG CCACAGGTCG CTGCGAAACG 180
 5 GCGGACCGCT CCAAAGCGCG CCGTGGATGG GATCGCCGAG CAGTTCGTGC AGCTCCAGG 240
 AACGTTGCGA ATGCAGCGCG CCGAGGCTCA GGCCATGCAG ATACAGGCGC GGTGCGCGTT 300
 CGGCCGGCAG TTCGGTCCAG TAGCCATAGA TCTCGGCGAA TAGCGCGCGG GCCACGTCGC 360
 GGCCGTAGTC GGCCTCCACC AGCAGCGCCA GCGGGCTGTT CAGATAGGAG TACTGCAACG 420
 CCACGCTGGC GATATCGCCG TGGTGCAGGT ATTCCACTGC GTTCATCGCC GCCGGGTCGA 480
 10 TCCAGCCGGT ACCGGTGGGC GTCACCAGCA CCAGCACCGA TCGCTCGAAG GCGCCGCTGC 540
 GCTGCAGCTC GCGCAAGGCC AGACGCGCCC GCTGGCGCGG GGTCTCTGCC GCGCGCAGAC 600
 CGACGTAGAC GCGAATCGGC TCGAGCGCCG AGCGGCGGCT CAAGACGCTG ATATCCGCCG 660
 CCGACGGGCC GGAGCCGATG AACTCGCGGC CCGTGGCGCC CAGCTCCTCC CAGCGCAGCA 720
 ACGAGGCCCC GCTGCCGCTT TTCAGCGCGC AGGCCGGTGG CGCCGTCTCC GGTTCGATCA 780
 15 GGGCGTCGTA CTGCGCGAAG GATGCGTCCA GCATGCGCAG TGCCCGCGCC GCCAGCACAT 840
 CGTGAGCAG CGACCAGAAC AGCGCCAGCG CCACCAGCAC GCCGATCAGC TTGGCCAGGC 900
 GCCGTGGCAG CACGCGGTCG GCGTCCCGCG AGACGAAGCG CGACACCAGC CGATACAGAC 960
 GCGCCAGCGT CAGCAGGATG AGAAAGGTCG CCAGCGCGGT GAGAATGACT TCGAGCAGGT 1020
 GCGCACTGCT CACCGGCGGC ATGCCCATCA GCGCGCGTAC CGCGTTCTGC CAGCCGGCGA 1080
 20 CCTGGCTGAG GAAATACCGG GCCAGCAGCA GGCAGCCGAC CGCGATCAGC AGATTGACCC 1140
 GCTCGCGCTG CCAGCGTGGG CGCTCCGGCA GTTCCAGATA GCGCCACAGC CAGCGCCAGA 1200
 ACACGCGGAG GCCATAGCCC ACCGCCAGCG CCGCGCCGGC CAGCACGCCC TGGCTCAGCG 1260
 TCGAGCGCGG CAGCAGCGAT GCGGTCAGCG CCGCGCAGAA GAACAGCGTG CCCAGCAGCA 1320
 GGCCGAAACC GGACAGCGAG CGCCAGATAT AGAGGACGGG CAGGTGCAGC ATGAAGATCT 1380
 25 CCGCGGTCCG GTGACGGCGT CGCGCCTCGG CATATCGAGG CGTGTCCGGT CGTGCGGTTC 1440
 CCGTGATGGT CCGCAGCAGG CCAATCCGAT GCAACGATGG CCGAGCGGCC GACTCAAACG 1500
 TCTACATTTC CCTAGTGCTG CCGGAACCGA TCGCCG 1536
 ATG AGC ATC CCA GAC AAC ACC TAT ATC GAA TGG CTG GTC AGC CAG TCC 1584
 ATG CTG CAT GCG GCC CGC GAG CGG TCG CGT CAT TAC GCC GGC CAG GCG 1632
 30 CGT CTC TGG CAG CGG CCT TAT GCC CAG GCC CGC CCG CGC GAT GCC AGC 1680
 GCC ATC GCC TCG GTG TGG TTC ACC GCC TAT CCG GCG GCC ATC ATC ACG 1728
 CCG GAA GGC GGC ACG GTA CTC GAG GCC CTC GGC GAC GAC CGC CTC TGG 1776
 AGT GCG CTC TCC GAA CTC GGC GTG CAG GGC ATC CAC AAC GGG CCG ATG 1824

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	AAG CGT TCC GGT GGC CTG CGC GGA CGC GAG TTC ACC CCG ACC ATC GAC	1872
	GGC AAC TTC GAC CGC ATC AGC TTC GAT ATC GAC CCG AGC CTG GGG ACC	1920
	GAG GAG CAG ATG CTG CAG CTC AGC CGG GTG GCC GCG GCG CAC AAC GCC	1968
	ATC GTC ATC GAC GAC ATC GTG CCG GCA CAC ACC GGC AAG GGT GCC GAC	2016
5	TTC CGC CTC GCG GAA ATG GCC TAT GGC GAC TAC CCC GGG CTG TAC CAC	2064
	ATG GTG GAA ATC CGC GAG GAG GAC TGG GAG CTG CTG CCC GAG GTG CCG	2112
	GCC GGG CGT GAT TCG GTC AAC CTG CTG CCG CCG GTG GTC GAC CCG CTC	2160
	AAG GAA AAG CAC TAC ATC GTC GGC CAG CTG CAG CGG GTG ATC TTC TTC	2208
	GAG CCG GGC ATC AAG GAC ACC GAC TGG AGC GTC ACC GGC GAG GTC ACC	2256
10	GGG GTC GAC GGC AAG GTG CGT CGC TGG GTC TAT CTG CAC TAC TTC AAG	2304
	GAG GGC CAG CCG TCG CTG AAC TGG CTC GAC CCG ACC TTC GCC GCG CAG	2352
	CAG CTG ATC ATC GGC GAT GCG CTG CAC GCC ATC GAC GTC ACC GGC GCC	2400
	CGG GTG CTG CGC CTG GAC GCC AAC GGC TTC CTC GGC GTG GAA CGG CGC	2448
	GCC GAG GGC ACG GCC TGG TCG GAG GGC CAC CCG CTG TCC GTC ACC GGC	2496
15	AAC CAG CTG CTC GCC GGG GCG ATC CGC AAG GCC GGC GGC TTC AGC TTC	2544
	CAG GAG CTG AAC CTG ACC ATC GAT GAC ATC GCC GCC ATG TCC CAC GGC	2592
	GGG GCC GAT CTG TCC TAC GAC TTC ATC ACC CGC CCG GCC TAT CAC CAT	2640
	GCG TTG CTC ACC GGC GAT ACC GAA TTC CTG CGC ATG ATG CTG CGC GAA	2688
	GTG CAC GCC TTC GGC ATC GAC CCG GCG TCA CTG ATC CAT GCG CTG CAG	2736
20	AAC CAT GAC GAG TTG ACC CTG GAG CTG GTG CAC TTC TGG ACG CTG CAC	2784
	GCC TAC GAC CAT TAC CAC TAC AAG GGC CAG ACC CTG CCC GGC GGC CAC	2832
	CTG CGC GAA CAT ATC CGC GAG GAA ATG TAC GAG CGG CTG ACC GGC GAA	2880
	CAC GCG CCG TAC AAC CTC AAG TTC GTC ACC AAC GGG GTG TCC TGC ACC	2928
	ACC GCC AGC GTG ATC GCC GCG GCG CTT AAC ATC CGT GAT CTG GAC GCC	2976
25	ATC GGC CCG GCC GAG GTG GAG CAG ATC CAG CGT CTG CAT ATC CTG CTG	3024
	GTG ATG TTC AAT GCC ATG CAG CCC GGC GTG TTC GCC CTC TCC GGC TGG	3072
	GAT CTG GTC GGC GCC CTG CCG CTG GCG CCC GAG CAG GTC GAG CAC CTG	3120
	ATG GGC GAT GGC GAT ACC CGC TGG ATC AAT CGC GGC GGC TAT GAC CTC	3168
	GCC GAT CTG GCG CCG GAG GCG TCG GTC TCC GCC GAA GGC CTG CCC AAG	3216
30	GCC CGC TCG CTG TAC GGC AGC CTG GCC GAG CAG CTG CAG CGG CCA GGC	3264
	TCC TTC GCC TGC CAG CTC AAG CGC ATC CTC AGC GTG CGC CAG GCC TAC	3312
	GAC ATC GCT GCC AGC AAG CAG ATC CTG ATT CCG GAT GTG CAG GCG CCG	3360
	GGA CTC CTG GTG ATG GTC CAC GAG CTG CCT GCC GGC AAG GGC GTG CAG	3408

CTC ACG GCA CTG AAC TTC AGC GCC GAG CCG GTC AGC GAG ACC ATC TGC 3456
 CTG CCC GGC GTG GCG CCC GGC CCG GTG GTG GAC ATC ATT CAC GAG AGT 3504
 GTG GAG GGC GAC CTC ACC GAC AAC TGC GAG CTG CAG ATC AAC CTC GAC 3552
 CCG TAC GAG GGG CTT GCC CTG CGT GTG GTG AGC GCC GCG CCG CCG GTG 3600
 5 ATC TGA GCGC 3610
 CCTCTTCGCG CGCCCCGGGT CCGCCGCTAT AGTGCGCAGC GCCTGGGGCG CGCATTGCCC 3670
 TCGCCGTCGA GACCAGCCCG TGTCGTTTAC TTCGCTTTTC CGCCTTGCGC TGCTGCCGCT 3730
 GCGCTGCTT GCCGCACCCG TCTGGGCGCA GACCGCTGC CCGCCCGGCC AGCAGCCGAT 3790
 CTGCCTGAGC GGCAGCTGCC TCTGCGTGCC GGCCGCCGCC AGCGATCCAC AGGCGGTCTA 3850
 10 CGACCGCGTG CAGCGTATGG CTACGCTGGC CCGTGCAGAAC TGGATCCAGC AGTCGCGCGA 3910
 CCGCCTGATG GCCGGCGGCG TCGAGCCGAT ACCGCTGCAC ATCCGCTCGC AGCTCGAGCC 3970
 GTATTTTCGAT CTTGCCGTGC TGGAGAGTGC GCGGTACCGC GTCGGCGACG AGGTGGTGCT 4030
 GACTGCCGGC AACACCCTGC TGGCAACCC GGACGTCAAT GCCGTGACCC TGATCGACGT 4090
 CATCGTCTTC CGCCACGAGG AGGATGCCCG GGACAACGTC GCGCTCTGGG CCCATGAGCT 4150
 15 CAAGCACGTC GAGCAATATC TGGACTGGGG CGTCGCCGAG TTCGCCCGGC GCTATACGCA 4210
 GGATTTCCGT GCCGTGGAGC GCCCGGCCTA TGCCTGGAG CGTGAGGTGG AAGAGGCCCT 4270
 GCGCGAGACG CAGACGCGGC GCTGAGCGAG CTGATCGGTG CTGCTGCCCG CACTGGGCTG 4330
 AAGCCCACCA ATGACGCGCG CGAAAACGAA AAACCCCGCC GAGGCGGGGT TTCTGACGCG 4390
 GGTTGTGCGG TCAGCTCAGA ACGCCGGGAC CACGGCGCCC TTGTACTTTT CCTCGATGAA 4450
 20 CTGGCGTACT TGCTCGCTGT GCAGCGCGGC AGCCAGTTTC TGCATGGCAT CGCTGTCCTT 4510
 GTTGTCCGGA CGGGCGACCA GAATGTTTAC GTATGGCGAG TCGCTGCCCT CGATCACCAG 4570
 GGCGTCCTGG GTCGGGTTCA GCTTGCTTC CAGCGCGTAG TTGGTGTGTA TCAGCGCCAG 4630
 GTCGACCTGG GTCAGCACGC GCGGCAGAGT CGCGGCTTCC AGTTCGCGGA TCTTGATCTT 4690
 CTTCCGGGTC TCGGCGATGT CTTCCGGCTG GCGGTGATGC CGGCGCCGTC CTTCAGACCG 4750
 25 ATC 4753

3. A recombinant plasmid containing the trehalose synthase gene of claim 1.

30 4. The recombinant plasmid according to claim 1 which is recombinant plasmid pCJ122.

5. A transformed E. coli with the recombinant plasmid of claim 1.

6. The transformant according to claim 5 in which the recombinant plasmid is pCJ122.

7. A process for producing trehalose which comprises reacting the trehalose synthase enzyme of claim 1 with maltose solution to obtain trehalose.

8. A process for producing trehalose which comprises crushing the transformed E. coli of claim 5, centrifuging the crushed bacteria, and reacting the resulting supernatant with maltose solution to obtain trehalose.

9. A novel microorganism *Pseudomonas stutzeri* CJ38 that produces trehalose from maltose.

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